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FILE 'BIOSIS' ENTERED AT 16:54:22 ON 26 MAR 2004
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=> s gill.in.
L1        30277 GILL.IN.

=> s l1 and likelihood ratio#
L2            3 L1 AND LIKELIHOOD RATIO#

=> dup reml2
ENTER REMOVE, IDENTIFY, ONLY, OR (?):end

=> dup rem l2
PROCESSING COMPLETED FOR L2
L3             2 DUP REM L2 (1 DUPLICATE REMOVED)

=> d l3 1-2 bib ab kwic

L3   ANSWER 1 OF 2  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2003:128633  BIOSIS
DN   PREV200300128633
TI   Linkage of aggressive prostate cancer to chromosome 7q31-33 in German
     prostate cancer families.
AU   Paiss, Thomas; Woerner, Sonja; Kurtz, Florian; Haeussler, Juergen;
     Hautmann, Richard E.; Gschwend, Juergen E.; Herkommer, Kathleen; Vogel,
     Walther [Reprint Author]
CS   Department of Human Genetics, University of Ulm, 89081, Ulm, Germany
     walther.vogel@medizin.uni-ulm.de
SO   European Journal of Human Genetics, (January 2003) Vol. 11, No. 1, pp.
     17-22. print.
     ISSN: 1018-4813.
DT   Article
LA   English
ED   Entered STN: 5 Mar 2003
     Last Updated on STN: 5 Mar 2003
AB   It has been suggested that chromosome 7q32 contains genes that influence
     the progression of prostate cancer from latent to invasive disease.  In an
     attempt to confirm this linkage to prostate cancer aggressiveness, 100
     German prostate cancer families were genotyped using a panel of eight
     polymorphic markers on chromosome 7q.  We used a multipoint allele sharing
     method based upon a likelihood ratio test implemented
     in GENEHUNTERPLUS v1.2 in order to calculate the nonparametric Zlr and the
     associated LOD scores.  We applied the aggressiveness of prostate cancer
     given by the pathological tumour grade of each individual, and the mean
     age of onset of a family as covariates, and constructed two weighted
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models. The first (weight0-1 model) puts weights on families with at least two cases of **Gill** prostate cancer. The second (weight0-2 model) also adds weights to families with early and late onset cancer respectively. The unweighted analysis gave no evidence of linkage to chromosome 7q. The Zlr scores increased when including the covariates, to 2.60 (P=0.005) using the weight0-1 and to 3.02 (P=0.001) using the weight0-2 model for late onset prostate cancer. The associated LOD scores were respectively 1.47 (P=0.009) and 1.98 (P=0.002). The markers that gave most evidence for linkage were exactly in the range of the published prostate cancer aggressiveness region. Our results support a widespread relevance of this locus and suggest that aggressive and late onset prostate cancer is linked to chromosme 7q31-33 in the German population.

AB. . . using a panel of eight polymorphic markers on chromosome 7q. We used a multipoint allele sharing method based upon a **likelihood ratio** test implemented in GENEHUNTERPLUS v1.2 in order to calculate the nonparametric Zlr and the associated LOD scores. We applied the. . . covariates, and constructed two weighted models. The first (weight0-1 model) puts weights on families with at least two cases of **Gill** prostate cancer. The second (weight0-2 model) also adds weights to families with early and late onset cancer respectively. The unweighted. . .

L3 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
AN 2002:217889 CAPLUS
DN 136:228056
TI Application of GenePrint PowerPlex 16 system in analyzing of forensic mix stains
AU Wolanska-Nowak, Paulina; Branicki, Wojciech; Kupiec, Tomasz
CS Institute of Forensic Research, Krakow, Pol.
SO Z Zagadnien Nauk Sadowych (2001), 46, 116-124
CODEN: ZZSAF3; ISSN: 1230-7483
PB Instytut Ekspertyz Sadowych im. Prof. dra Jana Sehna
DT Journal
LA English
AB The use of STR Multiplexes has become a routine procedure in profiling forensic stains. The GenePrint PowerPlex 16 System allows the simultaneous coamplification and three-color detection of sixteen loci. It contains two new low-stutter, highly polymorphic pentanucleotide repeat loci, Penta E and Penta D, what makes it ideal for evaluation of DNA mixts. often encountered in forensic casework. The statistical treatment of mixed stains has been formulated in general math. approach by B.S. Weir et al. (1997). The strength of such evidence is represented by the **Likelihood Ratio**. The anal. requires the assignment of probabilities of all of the combinations of genotypes. Taking into consideration the area of peaks enhances the interpretation of DNA mix stains but involves the need to consider possible artifacts such as stutters. DNA analyses were performed in the range of alleles included in PowerPlex 16 System. In the case when major/minor components cannot be distinguished, we used "dnamix" program of Weir. When the major/minor components can be established, the mixture proportions were estimated for all loci. The inference about suspect/victim match to the profile was described with **Likelihood Ratio**. We describe here three forensic cases where the above-mentioned analyses were successfully performed. At the first case the suspect set of alleles was find in the mix stain DNA profile taken from rubbery mask and the probability of this hypothesis was estimated At the second case, the victims set of alleles was found in the mixed DNA profile from the suspect's night suit. It was estimated that the explanation that it was the victim's material in the mixed profile was 50 000 more probable than under the hypothesis that it was of random origin. In the third case each of three assailants cell material were revealed in the mixed DNA profiles taken from three different fragments of stockings found at the crime scene. The presented examples of cases from our routine work examns. indicate usefulness of **likelihood ratio** approach, as theor. justified by I.W.

Evett and P.D. **Gill** (1998), to estimation the value of DNA evidence, in the case of mixed stain.

RE CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB The use of STR Multiplexes has become a routine procedure in profiling forensic stains. The GenePrint PowerPlex 16 System allows the simultaneous coamplification and three-color detection of sixteen loci. It contains two new low-stutter, highly polymorphic pentanucleotide repeat loci, Penta E and Penta D, what makes it ideal for evaluation of DNA mixts. often encountered in forensic casework. The statistical treatment of mixed stains has been formulated in general math. approach by B.S. Weir et al. (1997). The strength of such evidence is represented by the **Likelihood Ratio**. The anal. requires the assignment of probabilities of all of the combinations of genotypes. Taking into consideration the area of peaks enhances the interpretation of DNA mix stains but involves the need to consider possible artifacts such as stutters. DNA analyses were performed in the range of alleles included in PowerPlex 16 System. In the case when major/minor components cannot be distinguished, we used "dnamix" program of Weir. When the major/minor components can be established, the mixture proportions were estimated for all loci. The inference about suspect/victim match to the profile was described with **Likelihood Ratio**. We describe here three forensic cases where the above-mentioned analyses were successfully performed. At the first case the suspect set of alleles was find in the mix stain DNA profile taken from rubbery mask and the probability of this hypothesis was estimated At the second case, the victims set of alleles was found in the mixed DNA profile from the suspect's night suit. It was estimated that the explanation that it was the victim's material in the mixed profile was 50 000 more probable than under the hypothesis that it was of random origin. In the third case each of three assailants cell material were revealed in the mixed DNA profiles taken from three different fragments of stockings found at the crime scene. The presented examples of cases from our routine work examns. indicate usefulness of **likelihood ratio** approach, as theor. justified by I.W. Evett and P.D. **Gill** (1998), to estimation the value of DNA evidence, in the case of mixed stain.

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=> s whitatker.in.
L4            0 WHITATKER.IN.

=> s whitaker.in.
L5          781 WHITAKER.IN.

=> s l5 and likelihood ratio#
L6            0 L5 AND LIKELIHOOD RATIO#

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=> s Buckleton.in.
L7            1 BUCKLETON.IN.

=> d l7 bib ab kwic
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AN 1999327290 EMBASE

TI The robustness of a continuous likelihood approach to bayesian analysis of forensic glass evidence.

AU Curran J.M.; Buckleton J.; Triggs C.M.

CS J.M. Curran, Statistical Genetics, Department of Statistics, North Carolina State University, Box 8203, Raleigh, NC 27606-8203, United States. curran@stat.auckland.ac.nz

SO Forensic Science International, (1999) 104/2-3 (91-103).

Refs: 9
ISSN: 0379-0738 CODEN: FSINDR
PUI S 0379-0738(99)00097-3
CY Ireland
DT Journal; Article
FS 049 Forensic Science Abstracts
LA English
SL English
AB In previous work [1-3] the authors [K.A.J. Walsh, J.S. **Buckleton**, C.M. Triggs, A practical example of glass interpretation, Sci. Justice 36 (1996) 213-218; J.M. Curran, Forensic application of Bayesian interference to glass evidence, Ph.D. Thesis, Department of Statistics, University of Auckland, 1997; J.M. Curran, C.M. Triggs, J.S. **Buckleton**, S. Coulson, Combining a continuous Bayesian approach with grouping information, Forensic Sci. Int. 91 (1998) 181-196] have presented various aspects of a Bayesian interpretation of forensic glass evidence. Such an interpretation relies on assumptions that may not hold. This paper demonstrates the robustness of the Bayesian approach to deviations from the statistically convenient notion of normality of the measurements. Copyright (C) 1999 Elsevier Science Ireland Ltd.
AB In previous work [1-3] the authors [K.A.J. Walsh, J.S. **Buckleton**, C.M. Triggs, A practical example of glass interpretation, Sci. Justice 36 (1996) 213-218; J.M. Curran, Forensic application of Bayesian interference to glass evidence, Ph.D. Thesis, Department of Statistics, University of Auckland, 1997; J.M. Curran, C.M. Triggs, J.S. **Buckleton**, S. Coulson, Combining a continuous Bayesian approach with grouping information, Forensic Sci. Int. 91 (1998) 181-196] have presented various aspects. . .

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